

1 CCCACGCGTCCGGTCCGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA
 61 GCTCAAAGGGCCCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT
 121 CCAGAAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG
 181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC
 241 TGAGAGAGTTCTGGGTGTCTTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
 301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTG
 361 ATGACAAACCAATTTCCTCGATGATGTGCTTCTGAGTGTCTGCTGAGGAACAATGGGA
 421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCTCTGTCCAAGGC
 481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT
 541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTGCTGAGACTCGGGGAGCCATTGACCATCGTC
 601 TCTGAGGATGGAGACTGGTGGACGGTGTCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
 661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCTGATGAGGGCAG
 721 AAAGCAGAGGAAGTGTGTTGTTACCTGGGAACCTGGAGGGGCCCTTCTCATCCGGGAG
 781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTGTCAGTCCGCCTCAGCCGCCCTGCATCCTGG
 841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG
 901 CGCCTCACCTTCCCTCACTCCAGGCCCTGGTGGACCATTAATCTGAGCTGGCGGATGAC
 961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTGCAGAGGGCTGGCCCGCTCCCTGGCAAG
 1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC
 1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
 1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
 1201 GCCCAAAGGAGAGGCCAAAAGGGAACCAAGGCTGCACACCTAGAACCCCAATTGAGCCT
 1261 CCTGGGCACCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC
 1321 ATCTAGGGTCCACCTGTACCCTTGCTCTTTCTCTCTTAGCCCTTAGAAGTCACCTACT
 1381 TCCTTCCAGTGCCATGATCCCACCTGCGACCTCTAGTGCGAGTGCGAGAGAAGGTGGGACC
 1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG
 1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
 1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
 1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT
 1681 GGCCTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCCTAGCAGCAGATCTTGGATGG
 1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCTCTAA
 1801 ATGTCCCCCATTTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTTTGGAGACGGAGTCTT
 1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC
 1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
 1981 CACCATGCCTGGCTAATTTTTTTGTATTTTTTAGTAGACATGGGGTTTACCACATTGGCC
 2041 AGGCTGGTGTGCAACTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG
 2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTTCATTTTGTG
 2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
 2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
 2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC
 2341 CCTTGATTTCCCTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
 2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCTCTACTGGTTC
 2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA
 2521 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAA

FIG. 1



1 CCCACGCGTCCGGTCCGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA
61 GCTCAAAGGGCCCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT
121 CCAGAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG
181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC
241 TGAGAGAGTTCTGGGTGTCTTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCAAGCCTTTG
361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA
1 M G

421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGC
3 S L P S R R K S L P S P S L S S S V Q G

481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT
23 Q G P V T M E A E R S K A T A V A L G S

541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTGCTGAGACTCGGGGAGCCATTGACCATCGTC
43 F P A G G P A E L S L R L G E P L T I V

601 TCTGAGGATGGAGACTGGTGGACGGTGTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
63 S E D G D W W T V L S E V S G R E Y N I

661 CCCAGCGTCCACGTGGCCAAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG
83 P S V H V A K V S H G W L Y E G L S R E

721 AAAGCAGAGGAACTGCTGTTGTTACCTGGGAACCCCTGGAGGGGCCTTCCTCATCCGGGAG
103 K A E E L L L L P G N P G G A F L I R E

781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTGCTAGTCCGCTCAGCCGCCCTGCATCCTGG
123 S Q T R R G S Y S L S V R L S R P A S W

841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG
143 D R I R H Y R I H C L D N G W L Y I S P

901 CGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTA TCTGAGCTGGCGGATGAC
163 R L T F P S L Q A L V D H Y S E L A D D

961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTGCTGAGAGGGCTGGCCCGCTCCCTGGCAAG
183 I C C L L K E P C V L Q R A G P L P G K

1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC
203 D I P L P V T V Q R T P L N W K E L D S

1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
223 S L L F S E A A T G E E S L L S E G L R

1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
243 E S L S F Y I S L N D E A V S L D D A *

1201 GCCCAAAGGAGAGGGCCAAAAGGGAAACCAAGGCTGCACACCTAGAACCCCAATTACGCCT
1261 CCTGGGCACCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC
1321 ATCTAGGGTCCCACCTGTACCCTTGCTTTTCCCTCTCTTAGCCCTTAGAAGTCACTACT
1381 TCCTTCCAGTGCCATGATCCCACCTGCGACCTCTAGTGCGAGTGCGAGAGAAGGTGGGACC
1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTGTGACCTAGTTAGTTCTTG
1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT

FIG. 3A

1681 GGCTAGAAAGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGG
1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCCTCAA
1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTTTGAGACGGAGTCTT
1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC
1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
1981 CACCATGCCTGGCTAATTTTTTTGTATTTTGTAGATAGATGGGGTTTACCACATTGGCC
2041 AGGCTGGTGTGCAACTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAGTGCTG
2101 GGATTACAGTGTGTAGCCACGGCACCAGCCTAGCTCTCAGATCTCTATTTTCATTTTGTG
2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCGAG
2341 CTTTGATTTCCCTGCTGCCTCCATAAACGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
2401 AGGGAGAGGAGAAAGAGGGATGGGGTGGGAGGCACCCCCTCCAGTGCTCCTACTGGTTT
2461 CCAAGTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA
2522 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 3B

Homology	Amino acid level	
	Similarity	Identity
human SLAP x mouse SLAP	89.9%	88.0%
human SLAP x human SLAP-2	58.4%	47.4%
mouse SLAP x human SLAP-2	70.0%	58.1%

FIG. 4

```

hSLAP-2      1 MGSLPSRRKSLPSPSLSSSVQGGPVTMEAERSKATAVALGSFPAGGPAE
               : . |||. . :|. | :|. .
hSLAP        1 ...MGNSMKSTPAPA.....ERLPNPEGLDSDFLAVLSDYPSPDISP

51 LSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLS
   | | | :|:|:| | | :| .||| || :||:| | | | | |
41 PIFRRGEKLRVISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLG

101 REKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRI
   |:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
91 RDKAEELLQLPDTKVGSFMIRESETKKGFYSLSVR.....HRQVKHYRI

151 HCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCVLQIRAGPLP
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
135 FRLPNNWYYISPRLTFQCLEDLVNHYSEVADGLCCVLTTPCLTQSTAAPA

201 GKDIPLPVTVQRTPLNWK...ELDSSLLFSEAATG.EESLLSEGLRESLS
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
185 VRASSPVTLRQKTVDWRRVSRQLQEDPEGTENPLGVDESLSYGLRESIA

247 FYISLNDEAVSLDDA.....
   |:| | | . |
235 SYLSLTSEDNTSFDRKKKSISLMYGGSKRKSSFFSPPYFED

```

FIG. 5



hSLAP 1 MGNSMKSTPAPAERPLPNPEGLDSDFLAVLSDYPSDISPPIFRRGEKLR
||||||| |.|||| |. |||:|||||||.|||||||
mSLAP 1 MGNSMKSTSPPSERPLSSSEGLESDFLAVLTDYPSDISPPIFRRGEKLR

51 VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL
||||||| |.|||| |. |||:|||||||.|||||||
51 VISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL

101 PDKVGSFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF
||||:||||||| |. |||:|||||||.|||||||
101 PDKIGSFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF

151 QCLEDLVNHYSEVADGLCCVLTPCLTQSTAAPAVRAS.....SSPVTLR
||||||| |. |||:|||||||.|||||||
151 QCLEDLVTHYSEVADGLCCVLTPCLAQNI PAPTSHPSPTSPGSPVTLR

196 QKTVDWRRVSRLOEDPEGTENPLGVDESLSYGLRESIASYLSLTSEDNT
||| ||:||||||| || ||| |. |||:|||||||.|||||||
201 QKTFDWKRVSRLQEGSEGAENPLRVDESLSYGLRESIASYLSLTGDDSS

246 SFDRKKKSISL MYGGSKRKSSFFSPPYFED 276
|||||||:|||| |. |||:|||||||.|||||||
251 SFDRKKKSLSL MYTGSKRKSSFFSAPQYFED 281

FIG. 6

hSLAP-2

1 MG.SLPSRRKSLPS..PSLSSSVQGGPVTMEAERSKATAVALGSFPAGG
| | | : | | | | | : | : | | | : |

mSLAP

1 MGNSMKs..TSPPSERP.LSSS...EG...LE...SDFLAV.LTDYPS..

48 PAELS...LRLGEPLTIVSEDGDWWTVLSEVS.GRE.YNIPSVHVAKVSH
| : : | | | : : : | | : | | | | : | : | |
36 P.DISPPIFRRGEKLRVISDEGGWWKAIS.LSTGRESY.IPGICVARVYH

93 GWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYLSVRLSRPASW
| | : | | | : | | | | | | | | | : | : | | | | |
83 GWLFEGLGRDKAEELLQLPDTKIGSFMIRESKTKGFYLSVR.HR....

143 DRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCV
.: : | | | | | | | | | | | : | | | | | | : | | | |
128 .QVKHYRIFRLPNNWYYISPRLTFQCLEDLVTHYSEVADGLCCVLTTPCL

193 LQR..A.....GPL..PGKDIPLPVTV.QRTPLNWKELDSSLLFSEATG
| | | | | | | | | | | | | : | | | | | | | | | |
177 AQNIPAPTSHPSPTSPGS....PVTLRQKT.FDWKRV.SRL..QEGSEG

233 .E.....ESLLSEGLRESLSFYISL.NDEAVSLD
| | | | | | | | : | : | | | : | | |
219 AENPLRVDESLSFYGLRESIASYLSLTGDDSSSFD

FIG. 7

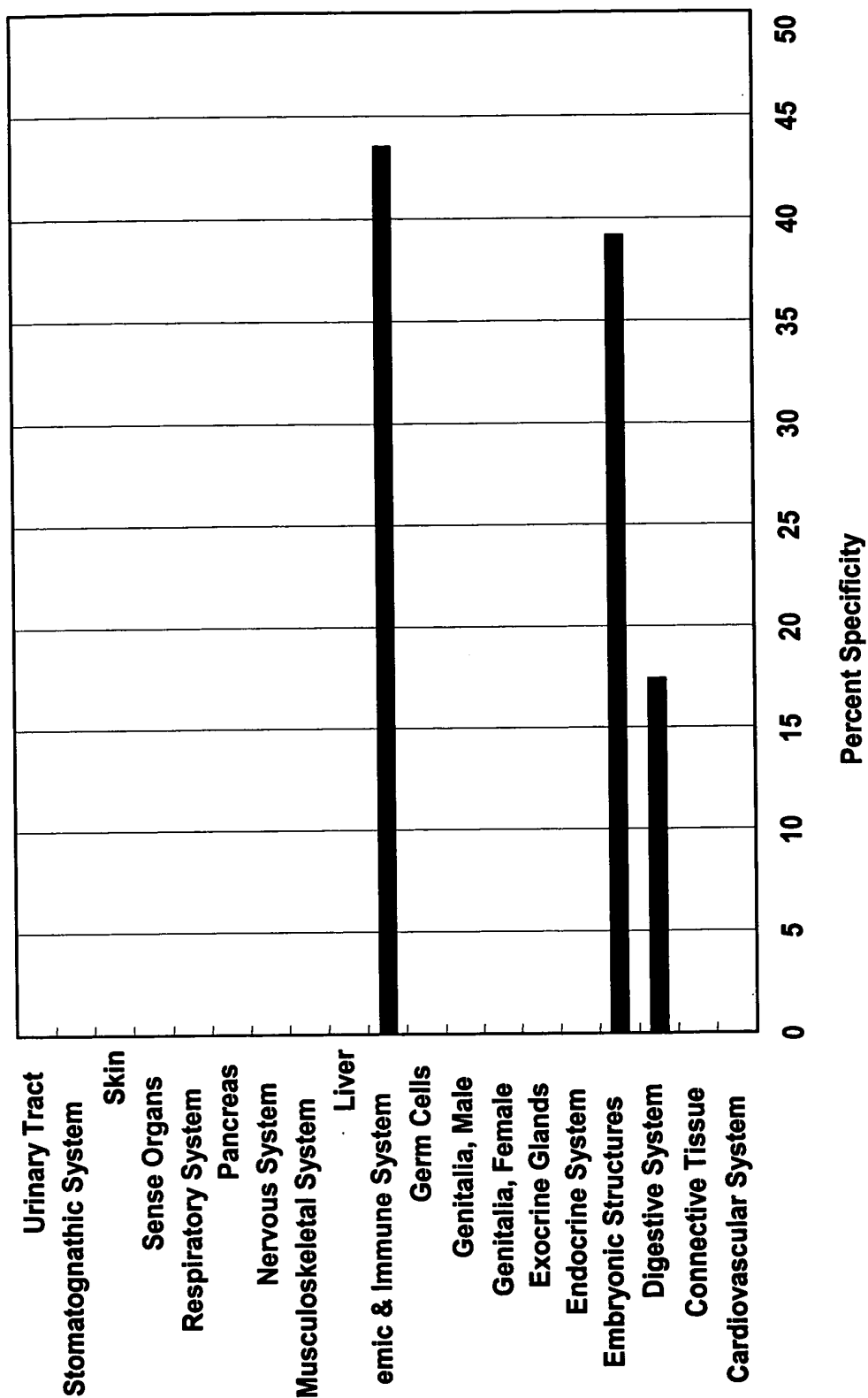


FIG. 8